

Please replace the paragraph on page 33, line 23 through page 34, line 15 of the specification with the following paragraph that has been re-written in clean form.

To carry out fine mapping of the *NPR1* gene, new CAPS and RFLP markers were generated from clones that the genetic maps in the AtDB database at Stanford's Arabidopsis genome website showed were located between *GAP-B* and *m315*. Cosmid *g4026* (CD2-28, *Arabidopsis* Biological Resource Center, The Ohio State University, Columbus, OH) was cut with the restriction enzyme *EcoRI* and a 4-kb fragment was used to identify a polymorphism between Col-0 and La-*er* after the genomic DNA was digested with *HindIII*. Using this RFLP marker, six heterozygotes were detected among the twenty-three F3 families that were heterozygous at *GAP-B*. None were found among the seven F3 families that were heterozygous at *m315*. Therefore, *g4026* is ~5.92 cm on the centromeric side of the *NPR1* gene. Cosmid *g11447* (obtained from the collection of Dr. Howard Goodman at the Massachusetts General Hospital (Nam et al., *Plant Cell* 1:699-705, 1989)) was used to generate a CAPS marker. End-sequences of an 0.8-kb *EcoRI* fragment were used to design PCR primers (primer 1: 5' GTGACAGACTTGCTCCTACTG 3' (SEQ ID NO:15); primer 2: 5' CAGTGTGTATCAAAGCACCA 3' (SEQ ID NO:16) which amplified a fragment displaying a polymorphism when digested with the *EcoRV* restriction enzyme. Among the 436 *npr1-1* F3 progeny tested using this newly generated CAPS marker, seventeen heterozygotes were discovered. Since these heterozygotes were all homozygous Col-0 for the *GAP-B* locus, the *g11447* marker was placed ~1.95 cM on the telomeric side of the *NPR1* gene.

Please replace the paragraph on page 35, lines 1-16, of the specification with the following paragraph that has been re-written in clean form.

A partial physical map of chromosome I at University of Pennsylvania's genomics website showed a YAC contig that includes *m305*. The YACs in this contig, as well as left-end-fragments of YAC clones yUP19H6, yUP21A4, and yUP11H9 were obtained from Dr. Joseph Ecker at the University of Pennsylvania. The yUP19H6L end-probe was found to

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detect an *Rsa*I polymorphism, and five recombinants were identified among the *GAP-B* recombinants on the centromeric side of the *NPR1* gene (as shown by the vertical arrows in Fig. 1). The yUP11H9L end-probe was found to detect a *Hind*III polymorphism, and one heterozygote was found among the seventeen recombinants for *gl447* on the telomeric side of the *NPR1* gene (as shown by a vertical arrow in Fig. 1). Since yUP11H9L hybridized with the yUP19H6 YAC clone, these results showed that the *NPR1* gene is located on yUP19H6. In addition to *m305*, yUP21A4L (detects an *Eco*RI polymorphism) and *g8020* (a 1.3-kb *Eco*RI fragment that detects a *Hind*III polymorphism) were found to be very closely linked to the *NPR1* gene with no recombinants identified. *m305*, yUP21A4L, and *g8020* all hybridized to the yUP19H6 YAC clone, further supporting the conclusion that yUP19H6 contains the *NPR1* gene.

Please replace the paragraph on page 42, line 14 through page 43, line 1 of the specification with the following paragraph that has been re-written in clean form.

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M13-20 and M13 reverse primers were used to initiate the sequencing reactions of the *Hind*III fragments. Various restriction enzymes were then used to generate deletions in these *Hind*III subclones to analyze sequences more distal to the ends of the fragments. In addition, primers were designed to perform primer walking. The relative positions of these *Hind*III fragments were determined and gaps between these fragments were filled by sequencing analyses using *Xba*I-subclones of cosmid 21A4-P5-1 as templates. The sequence data were analyzed to identify restriction enzyme sites, to perform sequence alignment and to search for open reading frames using standard DNA analysis software (DNA Strider 1.1, MacVector 4.0.1, and GeneFinder). Using this software only one putative gene was found. Sequence data were also compared to the TIGR *Arabidopsis thaliana* DataBase using the TIGR website. The results of this study identified an expression sequence tagged (EST) clone that showed homology with a portion of the 1.96-kb fragment. This portion of the 1.96-kb fragment was also identified as part of the gene recognized using GeneFinder software. The nucleotide sequence of the 7.5-kb genomic region encoding the *NPR1* gene product is shown in Fig. 4.